

#5

4-31452A.ST25.txt SEQUENCE LISTING

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Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu 50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser 65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn Page 34

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Lys	Asp				Thr					Lys	Cys	_	Ser 430	Gln	Ile
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Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met 485 490

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<211> 1743

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Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu 100 105 110

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Page 47

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ctt 44	gct	aca	gtt	tca	gtt	ttg	gct	gct	gca	ggc	agt	ttg	gct	cca	ata	13
	Ala	Thr	Val	Ser	Val	Leu	Ala	Ala	Ala	Gly	Ser	Leu	Ala	Pro	Ile	
		435					440					445				
tct 92	gga	aca	gtt	caa	agt	gct	cat	ctt	att	ata	aga	ttt	gac	gaa	aat	13
Ser	Gly	Thr	Val	Gln	Ser	Ala	His	Leu	Ile	Ile	Arg	Phe	Asp	Glu	Asn	
	450					455					460				,	
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	Val	Leu	Leu	Asn	Asn	Ser	Phe	Leu	Asp	Pro	Glu	Tyr	Trp	Asn	Phe	
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	Asn	Gly	Asp	Leu	Thr	Glu	Gly	Thr	Ala	Tyr	Thr	Asn	Ala	Val	Gly	
				485					490					495		
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36								JZA.	0125	. LAL						
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aaa	agt	aac	att	gtc	agt	caa	gtt	tac	tta	aac	qqa	qac	aaa	act	aaa	15
84								Tyr								
-		515					520	•			2	525	-2		-1-	
												020				
cct 32	gta	aca	cta	acc	att	aca	cta	aac	ggt	aca	cag	gaa	aca	gga	gac	16
	Val	Thr	Leu	Thr	Ile	Thr	Leu	Asn	Gly	Thr	Gln	Glu	Thr	Gly	Asp	
	530					535					540					
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Thr	Thr	Pro	Ser	Ala	Tyr	Ser	Met	Ser	Phe	Ser	Trp	Asp	Trp	Ser	Gly	
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	Asn	Tyr	Ile	Asn	Glu	Ile	Phe	Ala	Thr	Ser	Ser	Tyr	Thr	Phe	Ser	
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<223> Codes for a mutated Human Adenovirus type 5 fiber protein.

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Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser 35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu 50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn 85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu 100 105 110

Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr 115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile 130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln 145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr 165 170 175

Ala	Ser	Pro	Pro	Leu	Thr	Thr	Ala	Thr	Gly	Ser	Leu	Gly	Ile	Asp	Leu
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Ala	Pro	Leu	His	Val	Thr	Asp	Asp	Leu	Asn	Thr	Leu	Thr	Val	Ala	Thr
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Gly	Pro	Gly	Val	Thr	Ile	Asn	Asn	Thr	Ser	Leu	Gln	Thr	Lys	Val	Thr
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Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala 245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val 260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln 275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn 290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu 305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile 325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro 340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp 355 360 365

Ser	Asn	Lys	Ala	Met	Val	Pro	Lys	Leu	Gly	Thr	Gly	Leu	Ser	Phe	Asp
	370					375					380				_

Ser	Thr	Gly	Ala	Ile	Thr	Val	Gly	Asn	Lys	Asn	Asn	Asp	Lys	Leu	Thr
385					390					395					400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile 420 425 430

Leu Ala Thr Val Ser Val Leu Ala Ala Ala Gly Ser Leu Ala Pro Ile 435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn 450 455 460

Gly Val Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe 465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala 500 505 510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys 515 520 525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp 530 535 540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
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Tyr Ile Ala Gln Glu 580

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<213> Artificial Sequence

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<223> Codes for a mutated Human Adenovirus type 5 fiber protein.

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<222> (1)..(1746)

<223>

<220>

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<222> (1378)..(1380)

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tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act ccc 96

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20

25

30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 44

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35

40

45

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	50					55					60						
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Lys	Met	Gly	Asn	Gly	Leu	Ser	Leu	Asp	Glu	Ala	Gly	Asn	Leu	Thr	Ser		
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caa 88	aat	gta	acc	act	gtg	agc	cca	cct	ctc	aaa	aaa	acc	aag	tca	aac		2
Gln	Asn	Val	Thr	Thr	Val	Ser	Pro	Pro	Leu	Lys	Lys	Thr	Lys	Ser	Asn	,	
				85					90					95			
ata 36	aac	ctg	gaa	ata	tct	gca	ccc	ctc	aca	gtt	acc	tca	gaa	gcc	cta		3
	Asn	Leu	Glu	Ile	Ser	Ala	Pro	Leu	Thr	Val	Thr	Ser	Glu	Ala	Leu		
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act 84	gtg	gct	gcc	gcc	gca	cct	cta	atg	gtc	gcg	ggc	aac	aca	ctc	acc		3
	Val	Ala	Ala	Ala	Ala	Pro	Leu	Met	Val	Ala	Gly	Asn	Thr	Leu	Thr		
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	Gln	Ser	Gln	Ala	Pro	Leu	Thr	Val	His	Asp	Ser	Lys	Leu	Ser	Ile		
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	Thr	Gln	Gly	Pro	Leu	Thr	Val	Ser	Glu	Gly	Lys	Leu	Ala	Leu	Gln		

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aaa	gag	ccc	att	tat	aca	caa	aat	gga	aaa	cta	gga	cta	aag	tac	ggg	6
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Cly	ma	ЦСи	Ory		лър	DET	GIII	GIY		Mec	GIII	цец	ASII		AId	
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gga 16	gga	cta	agg	att	gat	tct	caa	aac	aga	cgc	ctt	ata	ctt	gat	gtt	8
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270

265

260

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ggc 12	cct	ctt	ttt	ata	aac	tca	gcc	cac	aac	ttg	gat	att	aac	tac	aac	9
Gly	Pro	Leu	Phe	Ile	Asn	Ser	Ala	His	Asn	Leu	Asp	Ile	Asn	Tyr	Asn	
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Ala	Ile	Asn	Ala	Gly	Asp	Gly	Leu	Glu	Phe	Gly	Ser	Pro	Asn	Ala	Pro	
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Ser	Asn	гàг	Ala	Met	Val	Pro	Lys	Leu	Gly	Thr	Gly	Leu	Ser	Phe	Asp	
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Lys	Asp	Ala	Lys	Leu	Thr	Leu	Val	Leu	Thr	Lys	Cys	Gly	Ser	Gln	Ile	
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Leu	Ala	Thr	Val	Ser	Val	Leu	Ala	Val	Lys	Gly	Ser	Leu	Ala	Pro	Ile	
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<212> PRT

<213> Artificial Sequence

<220>

<223> Codes for a mutated Human Adenovirus type 5 fiber protein.

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Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser 35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu 50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser 65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn 85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu 100 105 110

Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr 115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile 130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln Page 71

155

160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr 165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu 180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly 195 200 205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr 210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr 225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala 245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val 260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln 275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn 290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu 305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile 325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro Page 72

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Ser	Asn 370	Lys	Ala	Met	Val	Pro 375	Lys	Leu	Gly	Thr	Gly 380	Leu	Ser	Phe	Asp
Ser 385	Thr	Gly	Ala	Ile	Thr 390	Val	Gly	Asn	Lys	Asn 395	Asn	Asp	Lys	Leu	Thr 400
Leu	Trp	Thr	Thr	Pro 405	Ala	Pro	Ser	Pro	Asn 410	Cys	Arg	Leu	Asn	Ala 415	Glu
Lys	Asp	Ala	Lys 420	Leu	Thr	Leu	Val	Leu 425	Thr	Lys	Cys	Gly	Ser 430	Gln	Ile
Leu	Ala	Thr 435	Val	Ser	Val	Leu	Ala 440	Val	Lys	Gly	Ser	Leu 445	Ala	Pro	Ile
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Gly 465	Val	Leu	Leu	Asn	Asn 470	Ser	Phe	Leu	Asp	Pro 475	Glu	Tyr	Trp	Asn	Phe 480
Arg	Asn	Gly	Asp	Leu 485	Thr	Glu	Gly	Thr	Ala 490	Tyr	Thr	Asn	Ala	Val 495	Gly
Phe	Met	Pro	Asn 500	Leu	Ser	Ala	Tyr	Pro 505	Lys	Ser	His	Gly	Lys 510	Thr	Ala
Lys	Ser	Asn 515	Ile	Val	Ser	Gln	Val 520	Tyr	Leu	Asn	Gly	Asp 525	Lys	Thr	Lys
Pro	Val	Thr	Leu	Thr	Ile	Thr		Asn Page		Thr	Gln	Glu	Thr	Gly	Asp

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Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly 545 550 560

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28					Thr											5
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gcc 76	tca	ccc	cct	cta	act	act	gcc	act	ggt	agc	ttg	ggc	att	gac	ttg	5
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Lys	Glu	Pro	Ile	Tyr	Thr	Gln	Asn	Gly	Lys	Leu	Gly	Leu	Lys	Tyr	Gly	
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72																0
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Page 76

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Met	Gln 130	Ser	Gln	Ala	Pro	Leu 135	Thr	Val	His	Asp	Ser 140	Lys	Leu	Ser	Ile
Ala 145	Thr	Gln	Gly	Pro	Leu 150	Thr	Val	Ser	Glu	Gly 155	Lys	Leu	Ala	Leu	Gln 160
Thr	Ser	Gly	Pro	Leu 165	Thr	Thr	Thr	Asp	Ser 170	Ser	Thr	Leu	Thr	Ile 175	Thr
Ala	Ser	Pro	Pro 180	Leu	Thr	Thr	Ala	Thr 185	Gly	Ser	Leu	Gly	Ile 190	Asp	Leu
Lys	Glu	Pro 195	Ile	Tyr	Thr	Gln	Asn 200	Gly	Lys	Leu	Gly	Leu 205	Lys	Tyr	Gly
Ala	Pro 210	Leu	His	Val	Thr	Asp 215	Asp	Leu	Asn	Thr	Leu 220	Thr	Val	Ala	Thr
Gly 225	Pro	Gly	Val	Thr	Ile 230	Asn	Asn	Thr	Ser	Leu 235	Gln	Thr	Lys	Val	Thr 240
Gly	Ala	Leu	Gly	Phe 245	Asp	Ser	Gln	Gly	Asn 250	Met	Gln	Leu	Asn	Val 255	Ala
Gly	Gly	Leu	Arg 260	Ile	Asp	Ser	Gln	Asn 265	Arg	Arg	Leu	Ile	Leu 270	Asp	Val

Ser	Tyr	Pro 275		Asp	Ala	Gln	Asn 280		Leu	Asn	Leu	Arg 285		Gly	Gln
Gly	Pro 290	Leu	Phe	Ile	Asn	Ser 295		His	Asn	Leu	Asp 300	Ile	Asn	Tyr	Asn
Lys 305	Gly	Leu	Tyr	Leu	Phe 310	Thr	Ala	Ser	Asn	Asn 315		Lys	Lys	Leu	Glu 320
Val	Asn	Leu	Ser	Thr 325	Ala	Lys	Gly	Leu	Met 330	Phe	Asp	Ala	Thr	Ala 335	Ile
Ala	Ile	Asn	Ala 340	Gly	Asp	Gly	Leu	Glu 345	Phe	Gly	Ser	Pro	Asn 350	Ala	Pro
Asn	Thr	Asn 355	Pro	Leu	Lys	Thr	Lys 360	Ile	Gly	His	Gly	Leu 365	Glu	Phe	Asp
Ser	Asn 370	Lys	Ala	Met	Val	Pro 375	Lys	Leu	Gly	Thr	Gly 380	Leu	Ser	Phe	Asp
Ser 385	Thr	Gly	Ala	Ile	Thr 390		Gly	Asn	Lys	Asn 395	Asn	Asp	Lys	Leu	Thr 400
Leu	Trp	Thr	Thr	Pro 405	Ala	Pro	Ser	Pro	Asn 410	Cys	Arg	Leu	Asn	Ala 415	Gl _i u
Lys	Asp	Ala	Lys 420	Leu	Thr	Leu	Val	Leu 425	Thr	Lys	Cys	Gly	Ser 430	Gln	Ile
Leu	Ala	Thr 435	Val	Ser	Val	Leu	Ala 440	Val	Lys	Gly	Ser	Leu 445	Ala	Pro	Ile
Ser	Gly 450	Thr	Val	Gln	Ser	Ala 455	His	Leu	Ile	Ile	Arg 460	Phe	Asp	Glu	Asn

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe 465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala 500 505 510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys 515 520 525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gln Glu Thr Gly Asp Thr Thr 530 540

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4-31452A.ST25.txt
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4-31452A.ST25.txt
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